

Efficient local strategies for vaccination and network attack

Petter Holme^{1,2,*}

¹Department of Physics, Umeå University, 901 87 Umeå, Sweden

²NORDITA, Blegdamsvej 17, 2100 Copenhagen, Denmark

We study how a fraction of a population should be vaccinated to most efficiently stop epidemics. We argue that only local information (about the neighborhood of specific vertices) is usable in practice, and hence we consider only local vaccination strategies. The efficiency of the vaccination strategies is investigated with both static and dynamical measures. Among other things we find that the most efficient strategy for many real-world situations is to iteratively vaccinate the neighbor of the previous vaccinee that has most links out of the neighborhood.

PACS numbers: 89.65.-s, 89.75.Hc, 89.75.-k

I. INTRODUCTION

Diseases spread over networks. The spreading dynamics are closely related to the structure of networks. For this reason network epidemiology has turned into of the most vibrant subdisciplines of complex network studies. (6; 11; 14) A topic of great practical importance within network epidemiology is the vaccination problem: How should a population be vaccinated to most efficiently prevent a disease to turn into an epidemic? For economic reasons it is often not possible to vaccinate the whole population. Some vaccines have severe side effects and for this reason one may also want to keep number of vaccinated individuals low. So if cheap vaccines, free of side effects, does not exist; then having an efficient vaccination strategy is essential for saving both money and life. If all ties within the population is known, then the target persons for vaccination can be identified using sophisticated global strategies (cf. (9)); but this is hardly possible for nation-wide (or larger) vaccination campaigns. In a seminal paper Cohen *et al.* (4) suggested a vaccination strategy that only requires a person to estimate which other persons he, or she, gets close enough to for the disease to spread to—i.e., to name the “neighbors” in the network over which the disease spreads. For network with a skewed distribution of degree (number of neighbors) the strategy to vaccinate a neighbor of a randomly chosen person is much more efficient than a random vaccination. In this work we assume that each individual knows a little bit more about his, or her, neighborhood than just the names of the neighbors: We also assume that an individual can guess the degree of the neighbors and the ties from one neighbor to another. This assumption is not very unrealistic—people are believed to have a good understanding of their social surroundings (this is, for example, part of the explanation for the “navigability” of social networks) (15).

Finding the optimal set of vaccinees is closely related to the attack vulnerability problem (1; 9). The major difference is the dynamic system that is confined to the network—disease spreading for the vaccination problem and information flow for the attack vulnerability problem. To be able to protect the network efficiently one needs to know the worst case attacking

scenario. Large scale network attacks are, presumably, based on local (rather than global) network information. So, a grave scenario would be in the network was attacked with the same strategy that is most efficient for vaccination. We will use the vaccination problem as the framework for our discussion, but the results applies for network attack as well.

II. PRELIMINARIES

In our discussion we will use two measures of network structure: The *clustering coefficient* C of the network defined as the ratio of triangles with respect to connected triples normalized to the interval $[0, 1]$. (3) If $C = 1$ there is a maximal number of triangles (given a set of connected triples); if $C = 0$ the graph has no triangles. We also measure the degree-degree correlations through the *assortative mixing coefficient* defined as (13)

$$r = \frac{4\langle k_1 k_2 \rangle - \langle k_1 + k_2 \rangle^2}{2\langle k_1^2 + k_2^2 \rangle - \langle k_1 + k_2 \rangle^2}, \quad (1)$$

where k_i is the degree of the i ’th argument of an edge in a list of the edges, and $\langle \cdot \rangle$ denotes average over that edge-list. We let N denote the number of vertices and M the number of edges.

III. THE NETWORKS

We will test the vaccination strategies we propose on both real-world and model networks. The first real-world network is a scientific collaboration network (12). The vertices of this network are scientists who have uploaded manuscripts to the preprint repository arxiv.org. An edge between two authors means that they have coauthored a preprint. We also study two small real-world social networks: One constructed from an observational study of friendships in a karate club, another based on an interview survey among prisoners. The edges of these small networks are, probably, more relevant for disease spreading than the arxiv network, but may suffer from finite size effects. The three model networks are: 1. The Holme-Kim (HK) model (8) that produces networks with a power-law degree distribution and tunable clustering. Basically, it is

*Electronic address: holme@tp.umu.se

TABLE I Statistics of the networks. Note that the arxiv, prison and seceder model networks are not connected—the largest connected components contains 48561, 58 and 2162(1) nodes respectively.

network	N	M	C	r
arxiv	58342	294901	0.420	+0.324
karate club	34	78	0.256	-0.476
prison	67	85	0.310	+0.161
HK	2000	4000	0.1753(1)	-0.0458(1)
seceder	2200	6600	0.266(1)	+0.012(2)
WS	2000	4000	0.4219(1)	-0.01267(2)

a Barabási-Albert (BA) type growth model based on preferential attachment (2)—just as the BA model it has one parameter $m = M/N$ controlling the average degree and one (additional) parameter $m_t \in [1, m]$ controlling the clustering. We will use $M = 2N = 4000$ and $m = m_t + 1 = 4$ giving the maximal clustering for the given N and M . 2. The networked seceder model, modeling social networks with a community structure and exponentially decaying degree distributions (7). Briefly, it works by sequentially updating the vertices by, for each vertex v , rewiring all v 's edges to the neighborhood of a peripheral vertex. With a probability r an edge of v can be rewired to a random vertex (so r controls the degree of community structure). We use the parameter values $M = 3N = 6600$, $r = 0.1$ and $10M$ iterations on an Erdős-Rényi network (5). 3. The Watts-Strogatz (WS) model (16) generates networks with exponentially decaying degree distributions and tunable clustering. The WS model starts from the vertices on a circular topology with edges between vertices separated by 1 to k steps on the circle. Then one goes through the edges and rewire one side of them to randomly selected vertices with a probability P . We use $P = 0.05$ and $M = kN = 2N = 4000$.

IV. THE STRATEGIES

Now we turn to the definition of the strategies. We assume a fraction f of the population is to be vaccinated. As a reference we consider random vaccination (RND, equivalent to site percolation). We use the above mentioned *neighbor vaccination* (RN \bar{B})—to vaccinate the neighbor of randomly chosen vertices—and the trivial improvement (10) if knowledge about the neighbors' degrees are included: Pick a vertex at random and vaccinate one (randomly chosen) of its highest-degree neighbors (we call it DEG). To avoid overvaccination of a neighborhood one can consider to vaccinate neighbors of a vertex v with a maximal number of edges out of v 's neighborhood (OUT). For all strategies except RND we also consider “chained” versions were one, instead of vaccinating a neighbor of a randomly chosen vertex, vaccinates a neighbor of the vertex vaccinated in the previous time step (if all neighbors are vaccinated a neighbor of a random vertex is chosen instead). For the acronyms of the chained versions a suffix “C” is added.

V. RESULTS AND ANALYSIS

The results of this paper are presented in three sections: First we study how the number of vertices in the largest connected subgraph S_1 depends on the fraction f of vaccinated vertices. Then we show that the conclusions from S_1 also hold for dynamical simulations of disease spreading. To interpret the results we also investigate S_1 for a fixed f as a function of the clustering and assortative mixing coefficients.

A. Static efficiency

As a static efficiency measure we consider the size of the average largest connected component of susceptible (non-vaccinated) vertices, S_1 . We average over $n_{\text{vac}} = 1000$ runs of the vaccination procedures. The model networks are also averaged over $n_{\text{net}} = 100$ network realizations. (Smaller or larger n_{vac} and n_{net} does not make any qualitative difference.) In Fig. 1 we display S_1 as a function of f . For all except the WS model network the DEG and OUT (chained and unchained versions) form the most efficient set of strategies. Within this group the order of efficiency varies: For the arxiv network the OUT strategy is more than twice as efficient as any other for $0.25 \lesssim f \lesssim 0.4$. For the HK and seceder model networks the chained strategies are considerably more efficient than the unchained ones. We note that the difference between the chained and unchained versions of OUT and DEG is bigger than between OUT and DEG (or OUTC and DEGC). OUT do converge to DEG in the limit of vanishing C but all networks we test have rather high clustering. Another interesting observation is that even if the degree distribution is narrow, such as for the seceder model of Fig. 1(e) (where $P(k) \sim \exp(-k)$) the more elaborate strategies are much more efficient than random vaccination. This is especially clear for higher f which suggests that the structural change of the network of susceptible vertices during the vaccination procedure is an important factor for the overall efficiency. For the WS model network the chained algorithms are performing poorer than random vaccination. This is in contrast to all other networks. We conclude that epidemiology related results regarding the WS model networks should be cautiously generalized to real-world systems.

B. Dynamic efficiency

Static measures of vaccination efficiency are potential oversimplifications—there is a chance that the interplay between disease dynamics and the underlying network structure has a significant role. To motivate the use of S_1 we also investigate the SIS and SIR models (6) on vaccinated networks. In the SIS model a vertex goes from “susceptible” (S) to “infected” (I) and back to S. In the SIR model is just the same, except that an infected vertex goes to the “removed” (R) state and remain there. The probability to go from S to I (per contact) is zero for vaccinated vertices and $\lambda = 0.05$ for the rest. The I state lasts $\delta = 2.5$ time steps. We use synchronous updating and one randomly chosen initially infected person. The disease

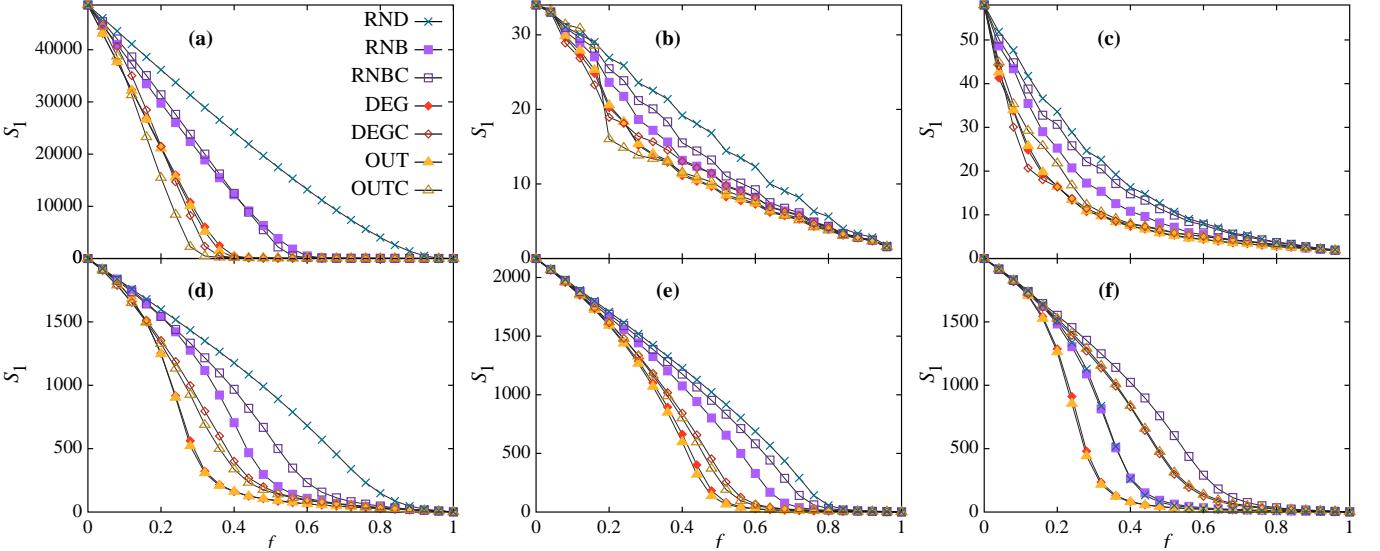


FIG. 1 The size of the largest connected component S_1 as a function of the fraction of vaccinated vertices for the (a) arxiv, (b) karate club, (c) prison, (d) HK model, (e) seceder model and (f) WS model network. Error bars are smaller than the symbol size. Lines are guides for the eyes.

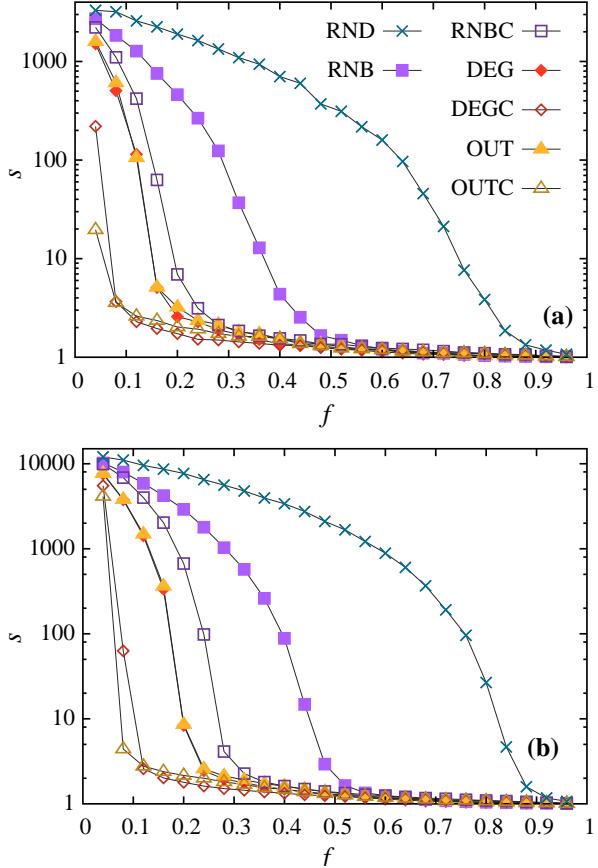


FIG. 2 The average number of vertices that are at least once infected during an outbreak s for (a) the SIR and (b) the SIS disease dynamics. Error bars of the order of the symbol size. Lines are guides for the eyes.

dynamics are averaged $n_{\text{dis}} = 100$ times for all $n_{\text{vac}} = 1000$ runs of the vaccination schemes. In Fig. 2(a) we plot the average number of individuals that at least once have been infected during an outbreak s —i.e., until there are no I-vertices left, or (for SIS) has reached an endemic state (defined in the simulations as when there are no susceptible vertices that have not had the disease at least once)—for the arxiv network. Other networks and simulation parameters give qualitatively similar results. Qualitatively, the large picture from the S_1 calculations remains—the chained and unchained DEG and OUT strategies are very efficient, and the chained versions are more efficient than the unchained. A difference is that the unchained RNB also performs rather well. Quantitatively, the differences between the strategies are huge, this is a result of the threshold behaviors of the SIS and SIR models (4). The conclusion of Fig. 2 (and similar plots for other networks) is that the order of the strategies' efficiencies are largely the same as concluded from the $S_1(f)$ -curves. But if high resolution is required, the measurement of network fragility has to be specific for the studied system.

C. The role of clustering and assortative mixing

To gain some insight how the network structure govern the relative efficiencies of the strategies we measure $S_1(f = 0.2)$ for varying assortative mixing and clustering coefficients. The results hold for other small f values. We keep the size and degree sequence constant to the values of the arxiv network. To perform this sampling we rewire pairs of edges (v_1, v_2) and (w_1, w_2) to (v_1, w_2) and (w_1, v_2) (unless this would introduce a self-edge or multiple edges). To ensure that the $n_{\text{rew}} = 100$ rewiring realizations are independent we start with rewiring $n_{\text{init}} = 3M$ pairs of edges. Then we go through pairs of edges randomly and execute only changes that makes the current

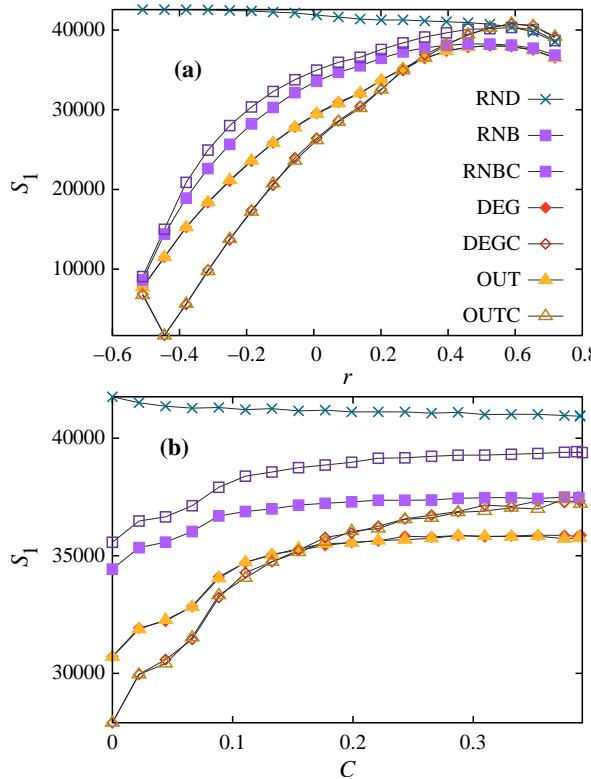


FIG. 3 How the size of the largest connected component vaccination of 20% of the population depends on clustering and degree-degree correlations. (a) shows $S_1(f = 0.2)$ plotted against r . (b) shows $S_1(f = 0.2)$ as a function of C . The networks have the same size and degree sequence as the arxiv network. Error bars are smaller than the symbol size. Lines are guides for the eyes.

r or C closer to their target values. When the value of r or C are within 0.1% of the target value the iteration is braked. The results seen in Fig. 3 shows that, just as before the OUT and DEG strategies, chained or unchained, are most efficient throughout the parameter space. The unchained versions are most efficient for $r \gtrsim 0.3$. An explanation is that, for high r , the chained versions will effectively only vaccinate the high-connected vertices (that are grouped together for very high r) and leave chains of low-degree vertices unvaccinated. The C -dependence plotted in Fig. 3(b) shows that the unchained versions outperform the chained versions for $C \gtrsim 0.15$. This is possibly a result of that the chains, for combinatorial reasons, get stuck in one part of the network. It is not an effect of biased degree-degree correlations since if the rewiring procedure is conditioned to a fixed r Fig. 3(b) remains essentially unaltered. We note that the structure of the original arxiv network differs from the rewired networks. For example, at $f = 0.2$ of Fig. 1(a) the OUT is 22% more efficient than OUTC, but in Fig. 3 the OUT and OUTC curves differ very little. For the RNB strategy the chained version is better than the unchained throughout the range of r and C values.

VI. SUMMARY AND CONCLUSIONS

To summarize, we have investigated strategies for vaccination and network attack that are based only on the knowledge of the neighborhood—information that humans arguably possess and utilize. Both static and dynamical measures of efficiency are studied. For most networks, regardless of the number of vaccinated vertices, the most efficient strategies are to choose a vertex v and vaccinate a neighbor of v with highest degree (DEG), or the neighbor of v with most links out of v 's neighborhood (OUT). v can be picked either as the lastly vaccinated vertex (chained selection) or at random (unchained selection). For real-world networks the chained versions tend to outperform the unchained ones, whereas this situation is reversed for the three types of model networks we study. We investigate the relative efficiency of chained and unchained strategies further by sampling random networks with a fixed degree sequence and varying assortative mixing and clustering coefficients. We find that the unchained strategies are preferable for networks with a very high clustering or strong positive assortative mixing (larger values than in seen in real-world networks). In Ref. (4) the authors propose the strategy to vaccinate a random neighbor of a randomly selected vertex. This strategy (RNB) requires less information of the neighborhood than DEG and OUT do. Thus the practical procedure gets simpler: One only has to ask a person “name a person you meet regularly” rather than “name the acquaintance of yours who meet most people you are not acquainted with regularly” (for OUT). (“Meet with regularly” should be replaced with some phrase signifying a high risk of infection transfer for the pathogen in question.) On the other hand, if the information of the neighborhoods is incomplete DEG and OUT will, effectively, be reduced to RNB (and thus not perform worse than RNB). To epitomize, choosing the people to vaccinate in the right way will save a tremendous amount of vaccine and side-effect cases. The best strategy can only be selected by considering both the structure of the network the pathogen spreads over, and the disease dynamics. If nothing of this is known the OUTC strategy our recommendation—it is better, or not much worse, than the best strategy in most cases. Together with DEGC, OUTC is most efficient for low clustering and assortative mixing coefficients, which is the region of parameter space for sexually transmitted diseases—the most interesting case for network based vaccination schemes (due to the well-definedness of sexual networks).

Acknowledgements

The author is grateful for comments from M. Rosvall and acknowledges support from the Swedish Research Council through contract no. 2002-4135.

References

- [1] R. Albert, H. Jeong, and A.-L. Barabási, *Attack and error tolerance of complex networks*, Nature **406** (2000), pp. 378-382.

- [2] A.-L. Barabási and R. Albert, *Emergence of scaling in random networks*, Science **286** (1999), pp. 509-512.
- [3] A. Barrat and M. Weigt, *On the properties of small-world network models*, Eur. Phys. J. B **13** (2000), pp. 547-560.
- [4] R. Cohen, S. Havlin, and D. ben Avraham, *Efficient immunization strategies for computer networks and populations*, Phys. Rev. Lett. **91** (2003), art. no. 247901.
- [5] P. Erdős and A. Rényi, *On random graphs I*, Publ. Math. Debrecen **6** (1959), pp. 290-297.
- [6] J. Giesecke, *Modern infectious disease epidemiology*, Arnold, London, 2 ed., 2002.
- [7] A. Grönlund and P. Holme, *Networking the seceder model: Group formation in social and economic systems*. e-print: cond-mat/0312010.
- [8] P. Holme and B. J. Kim, *Growing scale-free networks with tunable clustering*, Phys. Rev. E **65** (2002), art. no. 026107.
- [9] P. Holme, B. J. Kim, C. N. Yoon, and S. K. Han, *Attack vulnerability of complex networks*, Phys. Rev. E **65** (2002), art. no. 066109.
- [10] B. J. Kim, C. N. Yoon, S. K. Han, and H. Jeong, *Path finding strategies in scale-free networks*, Phys. Rev. E **65** (2002), art. no. 027103.
- [11] F. Liljeros, C. R. Edling, and L. A. Nunes Amaral, *Sexual networks: Implication for the transmission of sexually transmitted infection*, Microbes Infect. **5** (2003), pp. 189-196.
- [12] M. E. J. Newman, *The structure of scientific collaboration networks*, Proc. Natl. Acad. Sci. USA **98** (2001), pp. 404-409.
- [13] ———, *Assortative mixing in networks*, Phys. Rev. Lett. **89** (2002), art. no. 208701.
- [14] ———, *The structure and function of complex networks*, SIAM Rev. **45** (2003), pp. 167-256.
- [15] D. J. Watts, P. S. Dodds, and M. E. J. Newman, *Identity and search in social networks*, Science **296** (2002), pp. 1302-1305.
- [16] D. J. Watts and S. H. Strogatz, *Collective dynamics of 'small-world' networks*, Nature **393** (1998), pp. 440-442.